

DSP-5, encoded by 1020 base pairs

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1  GACGCGTGGC CATGTTGGAG GCTCCGGGCC CGAGTGATGG CTGCGAGCTC AGCAACCCCA
61  GCGCCAGCAG AGTCAGCTGT GCCGGGCAGA TGCTGGAAGT GCAGCCAGGA TTGTATTTCTG
121 GTGGGGCCGC GGCCGTCGCG GAGCCAGATC ACCTGAGGGA AGCGGGCATC ACGGCCGTGC
181 TAACAGTGGA CTCGGAGGAG CCCAGCTTCA AGGCGGGGCC TGGGGTCGAG GATCTATGGC
241 GCCTCTTCGT GCCAGCGCTG GACAAACCCG AGACGGACCT ACTCAGCCAT CTGGACCGGT
301 GCGTGGCCTT CATCGGTCAG GCCCGCGCTG AGGGCCGTGC GGTGTTGGTG CACTGTCATG
361 CAGGAGTCAG TCGAAGTGTG GCCATAATAA CTGCTTTTCT CATGAAGACT GACCAACTTC
421 CCTTTGAAAA AGCCTATGAA AAGCTCCAGA TTCTCAAACC AGAGGCTAAG ATGAATGAGG
481 GGTTTGAGTG GCAACTGAAA TTATACCAGG CAATGGGATA CGAAGTGGAT ACCTCTAGTG
541 CAATTTATAA GCAATATCGT TTACAAAAGG TTACAGAGAA GTATCCAGAA TTGCAGAATT
601 TACCTCAAGA ACTCTTTGCT GTTGACCCAA CTACCGTTTC ACAAGGATTG AAAGATGAGG
661 TTCTCTACAA GTGTAGAAAG TGCAGGCGAT CATTATTTCT AAGTTCTAGT ATTCTGGATC
721 ACCGTGAAGG AAGTGGACCT ATAGCCTTTG CCCACAAGAG AATGACACCA TCTTCCATGC
781 TTACCACAGG GAGGCAAGCT CAATGTACAT CTTATTTTCAT TGAACCTGTA CAGTGGATGG
841 AATCTGCTTT GTTGGGAGTG ATGGATGGAC AGCTTCTTTG CCCAAAATGC AGTGCCAAGT
901 TGGGTTTCCTT CAACTGGTAT GGTGAACAGT GCTCTTGTGG TAGGTGGATA ACACCTGCTT
961 TTCAAATACA TAAGAATAGA GTGGATGAAA TGAAAATATT GCCTGTTTTG GGATCACAAA
1021 CAGGAAAAAT ATGAACATGA TATTTTATAG CTTGGGAAGA AACTTGCAGA TGATATGTGC
1081 TGCCTTTGCT TCTTATCATT CATGGC

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Fig. 1

Alternate form of DSP-5, encoded by 897 base pairs

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1 GACGCGTGGC CATGTTGGAG GCTCCGGGCC CGAGTGATGG CTGCGAGCTC AGCAACCCCA
61 GCGCCAGCAG AGTCAGCTGT GCCGGGCAGA TGCTGGAAGT GCAGCCAGGA TTGTATTTTCG
121 GTGGGGCCGC GGCCGTCGCG GAGCCAGATC ACCTGAGGGA AGCGGGCATC ACGGCCGTGC
181 TAACAGTGGA CTCGGAGGAG CCCAGCTTCA AGGCGGGGCC TGGGGTCGAG GATCTATGGC
241 GCCTCTTCGT GCCAGCGCTG GACAAACCCG AGACGGACCT ACTCAGCCAT CTGGACCGGT
301 GCGTGCCCTT CATCGGTCAG GCCCGCGCTG AGGGCCGTGC GGTGTTGGTG CACTGTCATG
361 CAGGAGTCAG TCGAAGTGTG GCCATAATAA CTGCTTTTCT CATGAAGACT GACCAACTTC
421 CCTTTGAAAA AGCCTATGAA AAGCTCCAGA TTCTCAAACC AGAGGCTAAG ATGAATGAGG
481 GGTTTGAGTG GCAACTGAAA TTATACCAGG CAATGGGATA CGAAGTGGAT ACCTCTAGTG
541 CAATTTATAA GCAATATCGT TTACAAAAGG TTACAGAGAA GTATCCAGAA TTGCAGAATT
601 TACCTCAAGA ACTCTTTGCT GTTGACCCAA CTACCGTTTC ACAAGGATTG AAAGATGAGG
661 TTCTCTACAA GTGTAGAAAG TGCAGGCGAT CATTATTTTCG AAGTTCTAGT ATTCTGGATC
721 ACCGTGAAGG AAGTGGACCT ATAGCCTTTG CCCACAAGAG AATGACACCA TCTTCCATGC
781 TTACCACAGG GAGGCAAGCT CAATGTACAT CTTATTTTCAT TGAACCTGTA CAGTGGATGG
841 AATCTGCTTT GTTGGGAGTG ATGGATGGAC AGGTGAGAAC ACATTTTATT TTCTACAATT
901 TTATTTTATG ATCTATATTT TATTCCTTCT TGCATTTTAA GCTCTATTTT AACTAGTGTT
961 TTGCTCCATT TCTTAATTC TTTATTTCTG ATGATTATAT CTTTCTTGTG TAGATAA
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Fig. 2

DSP-5, predicted peptide sequence of 340 amino acids

MLEAPGPSDGCELSNPSASRVSCAGQMLEVQPGLYFGGAAVAEPDHLREAGITAVLTVDSEEPSFKAGP
GVEDLWRLFVPALDKPETDLLSHLDRCVAFIGQARAEGRAVLVHCHAGVSRVAIIITAFLMKTDQLPFEK
AYEKLQILKPEAKMNEGFQWLKLYQAMGYEVDTSIAIKYRLQKVTEKYPELQNLQELFAVDPTTVS
QGLKDEVLYKCRKCRSLFRSSILDHREGSGPIAFAHKRMTSSMLTTGRQAQCTSYFIEPVQWMESAL
LGVMGQQLCPKCSAKLGSFNWYGEQCSGRWITPAFQIHKNRVDKMLPVLGSQTGKI*

Fig. 3

Alternate form of DSP-5, predicted peptide sequence of 299 amino acids

MLEAPGPSDGCELSNPSASRVSCAGQMLEVQPGLYFGGAAVAEPDHLREAGITAVLTVDSEEPSFKAGP
GVEDLWRLFVPALDKPETDLLSHLDRCVAFIGQARAEGRAVLVHCHAGVSRVAIIITAFLMKTDQLPFEK
AYEKLQILKPEAKMNEGFQWLKLYQAMGYEVDTSIAIKYRLQKVTEKYPELQNLQELFAVDPTTVS
QGLKDEVLYKCRKCRSLFRSSILDHREGSGPIAFAHKRMTSSMLTTGRQAQCTSYFIEPVQWMESAL
LGVMGQVVRTHFIFYNFIL*

Fig. 4

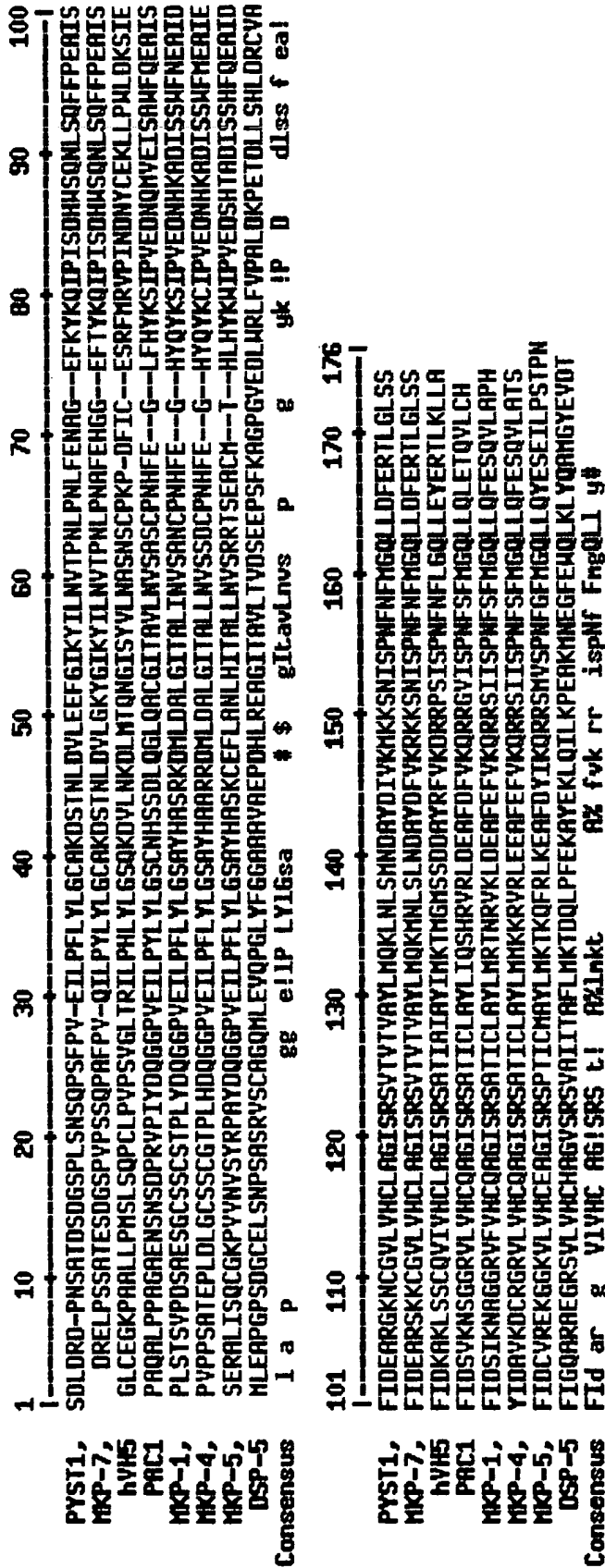
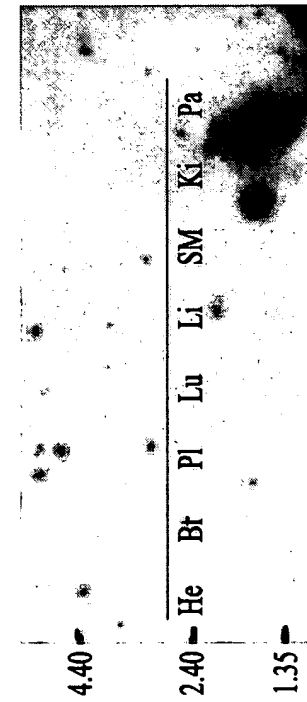


Fig. 5

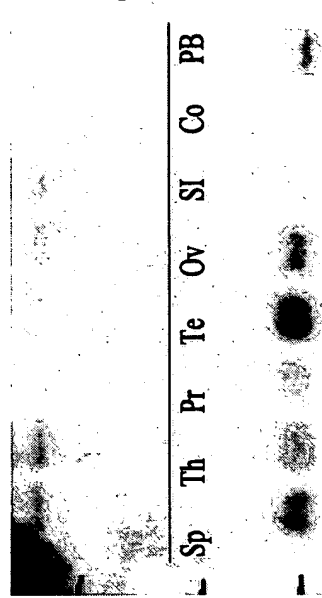
DSP-5

• Northern blot analysis



- He = Heart
- Br = Brain
- Pl = Placenta
- Lu = Lung
- Li = Liver
- SM = Skel. Muscle
- Ki = Kidney
- Pa = Pancreas

Fig. 6A



- Sp = Spleen
- Th = Thymus
- Pr = Prostate
- Te = Testis
- Ov = Ovaries
- SI = Small Intestine
- Co = Colon
- PB = Priph. Blood

Fig. 6B